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Maddox, Joyce R.
Rao, Aragula Gururaj
Crasta, Oswald R.
Folkerts, Otto
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 Val
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					tgc Cys											672
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gac Asp	caa Gln 370	ctc Leu	cgc Arg	gca Ala	gcc Ala	tac Tyr 375	gag Glu	aac Asn	gcc Ala	ggg ggg	gcc Ala 380	caa Gln	gtc Val	cca Pro	gag Glu	1152
ccg Pro 385	gcc Ala	aac Asn	gtg Val	ctc Leu	gaa Glu 390	atc Ile	gag Glu	tgg Trp	tcg Ser	aag Lys 395	cag Gln	cag Gln	tat Tyr	ttc Phe	caa Gln 400	1200
gga Gly	gct Ala	ccg Pro	agc Ser	gcc Ala 405	gtc Val	tat Tyr	Gly aaa	ctg Leu	aac Asn 410	gat Asp	ctc Leu	atc Ile	aca Thr	ctg Leu 415	ggt Gly	1248
tcg Ser	gcg Ala	ctc Leu	aga Arg 420	Thr	ccg Pro	ttc Phe	aag Lys	agt Ser 425	gtt Val	cat His	ttc Phe	gtt Val	gga Gly 430	acg Thr	gag Glu	1296
acg Thr	tct Ser	tta Leu 435	Val	tgg Trp	aaa Lys	gly aaa	tat Tyr 440	Met	gaa Glu	Gly aaa	gcc Ala	ata Ile 445	Arg	tcg Ser	ggt Gly	1344
caa Gln	cga Arg 450	ggt Gly	gct Ala	gca Ala	gaa Glu	gtt Val 455	Val	gct Ala	agc Ser	ctg Leu	gtg Val 460	Pro	gca Ala	gca Ala		1389
tag																1392

<sup>&</sup>lt;210> 11 <211> 463 <212> PRT

<sup>&</sup>lt;213> Exophiala spinifera

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			gaa Glu													144
			gtt Val													192
			act Thr			_	_		-	_		_	_		-	240
			aaa Lys													288
			gtg Val			_		_	_		-		_	_	_	336
			gcc Ala													384
			gga Gly													432
			gac Asp													480
			aga Arg 75													528
	_		gga Gly						_		_					576
			tat Tyr													624
			ctc Leu			-			_	_		_			_	672
			ctc Leu													720
			cac His 155													768

gl <sup>y</sup>	c gta y Val	a gca L Ala 170	a Asr	cag Glr	g ato 1 Ile	aca Thr	cgc Arg 175	, Ala	cto Lev	g cto Lei	ggt Gly	t gtg y Val	Glı	a gc	c cac a His	816
gag Glu	g ato 11e	e Sei	atg Met	ctt Leu	ttt Phe	ctc Leu 190	Thr	gac Asp	tac Tyr	ato Ile	aag Lys 195	s Ser	gco Ala	e aco	ggt Gly	864
cto Leu 200	ı Ser	aat Asr	att 1 Ile	ttc Phe	tcg Ser 205	Asp	aag Lys	aaa Lys	gac Asp	ggc Gly 210	Gl7	g cag ⁄Gln	tat Tyr	ato Met	g cga : Arg :215	912
tgo Cys	aaa Lys	aca Thr	ggt Gly	atg Met 220	Gln	tcg Ser	att Ile	tgc Cys	cat His 225	Ala	ato Met	j tca Ser	aag Lys	gaa Glu 230	ctt Leu	960
gtt Val	cca Pro	ggc	tca Ser 235	gtg Val	cac His	ctc Leu	aac Asn	acc Thr 240	ccc Pro	gtc Val	gct Ala	gaa Glu	att Ile 245	Glu	g cag Gln	1008
tcg Ser	gca Ala	tcc Ser 250	ggc	tgt Cys	aca Thr	gta Val	cga Arg 255	tcg Ser	gcc Ala	tcg Ser	ggc	gcc Ala 260	gtg Val	ttc Phe	cga Arg	1056
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aca Thr 280	ttt Phe	tca Ser	cca Pro	cct Pro	ctt Leu 285	ccc Pro	gcc Ala	gag Glu	aag Lys	caa Gln 290	gca Ala	ttg Leu	gcg Ala	gaa Glu	aat Asn 295	1152
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tgg Trp	tgg Trp	cgc Arg	gaa Glu 315	caa Gln	ggc Gly	ttc Phe	tcg Ser	ggc Gly 320	gtc Val	ctc Leu	caa Gln	tcg Ser	agc Ser 325	tgt Cys	gac Asp	1248
ccc Pro	atc Ile	tca Ser 330	ttt Phe	gcc Ala	aga Arg	Asp	acc Thr 335	agc Ser	atc Ile	gac Asp	gtc Val	gat Asp 340	cga Arg	caa Gln	tgg Trp	1296
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gcc Ala	tac Tyr	gag Glu	aac Asn	gcc Ala 380	ggg (	gcc ( Ala (	caa Gln	Val	cca Pro 385	gag Glu	ccg Pro	gcc Ala	Asn	gtg Val 390	ctc Leu	1440
gaa Glu	atc Ile	gag Glu	tgg Trp 395	tcg Ser	aag Lys (	cag ( Gln (	Gln '	tat Tyr 400	ttc Phe	caa Gln	gga Gly	Ala	ccg Pro 405	agc Ser	gcc Ala	1488
gtc	tat	aaa	ctg a	aac	gat (	ctc a	atc a	aca 1		ggt	tcg	gcg	ctc	aga	acg	1536

Val	Tyr	Gly 410	Leu	Asn	Asp	Leu	Ile 415	Thr	Leu	Gly	Ser	Ala 420	Leu	Arg	Thr	
_		_	_	_			_		_		_			gtt Val		1584
			-	-		_		_	-			-		gct Ala	_	1632
_	-	gtg Val	_	_		_		_	_	tagg	gegge	ecg (	2			1673

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190

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Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
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                                       210
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
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Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
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                              240
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
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Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
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                                          275
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
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                                       290
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
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               300
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
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Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
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Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
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                                          355
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
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Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
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Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
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                               400
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
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Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
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<212> DNA

<213> Unknown

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<221> misc feature

<222> (1)...(687)

<223> gst fusion + polylinker

<221> misc feature

<222> (688)...(2076)

<223> K:trAPAO

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<222> (688)...(690)

<223> Extra lysine

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	_										gat Asp 60		_	_		192
		_		_	_			_			gct Ala	_	_			240
	_			_				-	-		att Ile		_		_	288
		-	_	_		_			_	-	aga Arg		-		-	336
											agc Ser					384
											aaa Lys 140					432
-	_		_				_		_	_	tat Tyr	_	_		_	480
_	_			-	_		_	_	_	_	gcg Ala					528
_	_				_		_				caa Gln		-	_		576
_				_			_			_	cag Gln				_	624
_					_					_	gat Asp 220	_	-			672
		_	-			-		-		_	gtg Val	_				720
gct	ggc	ttg	agc	ggt	ttg	gag	acg	_	cgc 18	aaa	gtc	cag	gcc	gcc	ggt	768

Ala	. Gly	Leu	. Ser	Gly 245		Glu	Thr	Ala	Arg 250		: Val	. Gln	Ala	Ala 255	Gly	
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ctg Leu	agc Ser	gta Val 275	Gln	tcg Ser	ggt	ccc Pro	ggc Gly 280	Arg	acg Thr	act Thr	atc Ile	aac Asn 285	Asp	cto Leu	ggc	864
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gaa Glu 305	Arg	ttt Phe	cat His	ttg Leu	gag Glu 310	ggc	gag Glu	ctc Leu	cag Gln	agg Arg 315	acg Thr	act Thr	gga Gly	aat Asn	tca Ser 320	960
atc Ile	cat His	caa Gln	gca Ala	caa Gln 325	gac Asp	ggt Gly	aca Thr	acc Thr	act Thr 330	aca Thr	gct Ala	cct Pro	tat Tyr	ggt Gly 335	gac Asp	1008
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Ser	att Ile 450	tgc Cys	cat His	gcc Ala	atg Met	tca Ser 455	aag Lys	gaa Glu	ctt Leu	gtt Val	cca Pro 460	ggc Gly	tca Ser	gtg Val	cac His	1392
ctc Leu 465	aac Asn	acc Thr	ccc Pro	gtc Val	gct Ala 470	gaa Glu	att Ile	gag Glu	cag Gln	tcg Ser 475	gca Ala	tcc Ser	ggc Gly	tgt Cys	aca Thr 480	1440
gta Val	cga Arg	tcg Ser	gcc Ala	tcg Ser 485	ggc Gly	gcc Ala	gtg Val	Phe	cga Arg 490	agc Ser	aaa Lys	aag Lys	gtg Val	gtg Val 495	gtt Val	1488

			Thr			tat Tyr	Thr				Pro			1536
			500				505				510			
	_		_		_	ttg Leu	 _			_				1584
						tgg Trp 535								1632
						tcg Ser								1680
						gat Asp								1728
						aag Lys								1776
	_		_		_	caa Gln	_	_	_			_		1824
_		_			_	gcc Ala 615			_			_	_	1872
						gct Ala								1920
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Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
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Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
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Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
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Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
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Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
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Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
                                            620
                        615
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
                    630
                                        635
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
                645
                                    650
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
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Val Pro Ala Ala
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            for expression and secretion of the mature trAPAO
            in maize. Nucleotides 1-72, barley alpha amylase
            signal sequence, nucleotides 73-75, added lysine
            residue; nucleotides 76 -1464 , trAPAO cDNA.
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      <223> Added lysine residue
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                                                                       96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
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	c ctc p Leu		_					_	_			-	-	-		288
	a ttg g Leu															336
	a aat y Asn 90					_		_						_		384
	t ggt r Gly 5															432
	c ctc u Leu					_	-		_			_			_	480
	c aag u Lys															528
	c tac s Tyr															576
	c cag n Gln 170															624
	g ctt t Leu 5				_			_	_	_				_		672
	t ttc e Phe	_	_	_		_			_		_	_	_			720
	t atg y Met	_	_		_			_		_	_		-			768
	a gtg r Val															816
99	c tgt	aca	gta	cga	tcg	gcc	tcg		gcc	gtg	ttc	cga	agc	aaa	aag	864

Gly	Cys 250	Thr	Val	Arg	Ser	Ala 255	Ser	Gly	Ala	Val	Phe 260	Arg	Ser	Lys	Lys	
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cca Pro	cct Pro	ctt Leu	ccc Pro	gcc Ala 285	gag Glu	aag Lys	caa Gln	gca Ala	ttg Leu 290	gcg Ala	gaa Glu	aat Asn	tct Ser	atc Ile 295	ctg Leu	960
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gaa Glu	caa Gln	ggc Gly 315	ttc Phe	tcg Ser	ggc Gly	gtc Val	ctc Leu 320	caa Gln	tcg Ser	agc Ser	tgt Cys	gac Asp 325	ccc Pro	atc Ile	tca Ser	1056
ttt Phe	gcc Ala 330	aga Arg	gat Asp	acc Thr	agc Ser	atc Ile 335	gac Asp	gtc Val	gat Asp	cga Arg	caa Gln 340	tgg Trp	tcc Ser	att Ile	acc Thr	1104
tgt Cys 345	ttc Phe	atg Met	gtc Val	gga Gly	gac Asp 350	ccg Pro	gga Gly	cgg Arg	aag Lys	tgg Trp 355	tcc Ser	caa Gln	cag Gln	tcc Ser	aag Lys 360	1152
cag Gln	gta Val	cga Arg	caa Gln	aag Lys 365	tct Ser	gtc Val	tgg Trp	gac Asp	caa Gln 370	ctc Leu	cgc Arg	gca Ala	gcc Ala	tac Tyr 375	gag Glu	1200
aac Asn	gcc Ala	Gly 999	gcc Ala 380	caa Gln	gtc Val	cca Pro	gag Glu	ccg Pro 385	gcc Ala	aac Asn	gtg Val	ctc Leu	gaa Glu 390	atc Ile	gag Glu	1248
tgg Trp	tcg Ser	aag Lys 395	cag Gln	cag Gln	tat Tyr	ttc Phe	caa Gln 400	gga Gly	gct Ala	ccg Pro	agc Ser	gcc Ala 405	gtc Val	tat Tyr	gly aaa	1296
													ccg Pro			1344
agt Ser 425	gtt Val	cat His	ttc Phe	gtt Val	gga Gly 430	acg Thr	gag Glu	acg Thr	tct Ser	tta Leu 435	gtt Val	tgg Trp	aaa Lys	Gly aaa	tat Tyr 440	1392
atg Met	gaa Glu	gly	gcc Ala	ata Ile 445	cga Arg	tcg Ser	ggt Gly	caa Gln	cga Arg 450	ggt Gly	gct Ala	gca Ala	gaa Glu	gtt Val 455	gtg Val	1440
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<220> <221> SIGNAL <222> (1)...(24)

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425 Met	Glu	Gly	Ala	Ile 445	430 Arg	Ser	Gly	Gln	Arg 450	435 Gly	Ala	Ala	Glu	Val 455	440 Val	
Ala	Ser	Leu	Val 460	Pro	Ala	Ala										
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	< 2	220> 221> 222>		(2	1800]	)										
_	gca		gca	_	_	tac Tyr						-	_			48
~					_	ggc Gly	-			-						96
		_		_		gga Gly		_	_	_				-		144
						gcc Ala 55										192
						act Thr										240
		_	_		_	ccg Pro	_				-					288
~	_	_			_	ctt Leu	_					_	_	_		336
						tca Ser										384
						cac His 135										432
				_		ttg Leu	-		_		_	-	-		_	480
_	_	_		-		tgc Cys		_				_	_	_	_	528
		_		_	-	gta Val		_					_			576

	180		185		190	
	u Gly Ala		le Asn Asp	agc aac caa Ser Asn Gln 205		624
-	-	•		ggc gag ctc Gly Glu Leu 220		672
		-	_	ggt aca acc Gly Thr Thr 235		720
		Leu Leu Se		gtt gca agt Val Ala Ser		768
				gaa gag cat Glu Glu His		816
	rs Ala Ser		la Lys Arg	ctc gac agt Leu Asp Ser 285		864
				cct gct gtt Pro Ala Val 300		912
				gtg gaa gcc Val Glu Ala 315		960
		Thr Asp Ty	_	agt gcc acc Ser Ala Thr		1008
				cag tat atg Gln Tyr Met		1056
	et Gln Ser	· Ile Cys Hi		tca aag gaa Ser Lys Glu 365		1104
				gaa att gag Glu Ile Glu 380		1152
				gcc gtg ttc Ala Val Phe 395		1200
		Leu Pro Th	_	tat ccc acc Tyr Pro Thr	_	1248
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_				_	_	ata Ile	-		_		_	_	_		 1344
						ggc Gly 455									1392
		_	_	_		agc Ser		_	_	_	_				1440
	_		-	-		gac Asp	_			_				_	1488
						tct Ser									1536
						gtc Val			_	-					1584
		_	_	_	_	tat Tyr 535			~~	-	_	_	_	_	1632
	_		_			aca Thr	_		_			-	-	_	1680
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						cga Arg									1776
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<212> PRT

<213> Exophiala spinifera

<400> 23

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 6ly Val Gly Pro Asp Gly Gly Gly Arg Tyr Val 20
 20
 25
 30
 30

 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro 35
 40
 45
 45

 Ala Tyr Glu Lys Gln Val Ala Gln Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys 50
 55
 60

 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr 65
 70
 75
 80

 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val 100 105 110 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val 135 140 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val

Val	Ala	Ser 595			Pro	Ala	Ala 600						590	ı		
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		gcc Ala														96
		gtg Val														144
		gag Glu														192
		cct Pro														240
		ggt Gly														288

											ccc Pro					336
_	_		-	-	_						gtc Val 100					384
				_	_	_	_				ggt Gly			_	_	432
	~ ~								_		gct Ala	_		-	_	480
	_	_	_		_						aga Arg	_			_	528
			_	_		_					cag Gln	-		_		576
		_				_	_	_		_	cag Gln 180				_	624
_				_		_	-	_			ttt Phe		_	_		672
		_	_	_	_	_		_	_		atg Met					720
											gct Ala					768
	_		_	_		_					act Thr	_		_		816
	_			_		_		_	_	_	atg Met 260	_	_	_	_	864
	_		_	_		_					gga Gly					912
	_	_	_		_	_	_			_	tct Ser	_	_	_	_	960
											gtc Val					1008
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					gga Gly 350											1152
att Ile	gcc Ala	gcc Ala	att Ile	gag Glu 365	acc Thr	gag Glu	gta Val	aga Arg	ttc Phe 370	cag Gln	tgt Cys	cct Pro	tct Ser	gcc Ala 375	atc Ile	1200
					cgg Arg											1248
					gag Glu											1296
					gtc Val											1344
agt Ser 425	gcg Ala	acc Thr	gcc Ala	ttg Leu	gag Glu 430	gcc Ala	cag Gln	acg Thr	agc Ser	aaa Lys 435	tac Tyr	atg Met	cag Gln	ggt Gly	gcc Ala 440	1392
tgg Trp	gcg Ala	gcc Ala	ttt Phe	gcc Ala 445	aaa Lys	aac Asn	ccc Pro	atg Met	aat Asn 450	gly aaa	cct Pro	Gly 999	tgg Trp	aaa Lys 455	caa Gln	1440
					gcg Ala											1488
					aca Thr											1536
tat Tyr	tat Tyr 490	act Thr	gag Glu	ttg Leu	ggc Gly	aca Thr 495	atc Ile	gcg Ala	ccg Pro	agg Arg	aca Thr 500	ttt Phe	gly	gga Gly	ggc Gly	1584
					ggc Gly 510											1632
gta Val	gtg Val	gtg Val	ggc Gly	gct Ala 525	ggc	ttg Leu	agc Ser	ggt Gly	ttg Leu 530	gag Glu	acg Thr	gca Ala	cgc Arg	aaa Lys 535	gtc Val	1680
					tcc Ser											1728
gly aaa	gga Gly	aag Lys 555	act Thr	ctg Leu	agc Ser	gta Val	caa Gln 560	tcg Ser	ggt Gly	ccc Pro	ggc Gly	agg Arg 565	acg Thr	act Thr	atc Ile	1776

	_			_		tgg Trp 575			_				_	_	_	1824
						ttt Phe										1872
						caa Gln	_		_						_	1920
					_	ctg Leu	_			-	_	_	_			1968
_				_		tct Ser	_	_		_			_			2016
				_		cag Gln 655		_			_	_		_		2064
						gaa Glu			_		_	_			-	2112
						gct Ala										2160
						gac Asp										2208
						aaa Lys										2256
						tgc Cys 735										2304
						acc Thr										2352
						tcg Ser							_	_		2400
_			_	_		ccg Pro			_				_			2448
						gag Glu										2496
		795					800					805				

				aag Lys											254	4
				tcg Ser 830		_			-	_	-	_			259	)2
_	_			acc Thr											264	: O
				gga Gly											268	8
		-		aag Lys		_		_			_	-	_		273	6
				caa Gln											278	4
				cag Gln 910											283	2
				atc Ile											288	0
				gtt Val											292	8
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<213> Unknown

<220>

<221> SIGNAL

<222> (1)...(24)

<400> 25

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Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr 10 15 20

Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe

Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val

									<b>520</b>					F 2 F	
<i>α</i> 1	777	7.7.	~1	525	Ser	Crra	Lou	1727	530	Clu	ת דת	Mot	7 cm	535	Val
GIII	Ala	Ala	540	Leu	ser	Cys	ьеи	545	Leu	Giu	нта	Mec	550	Arg	vai
Glv	Glv	Lvs		Leu	Ser	Val	Gln		Glv	Pro	Glv	Arq		Thr	Ile
2	1	555					560		_		•	565			
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
	570					575					580				
	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu		Glu	Leu	Gln	Arg	
585	~ 3	_	_		590	~ 7		<b>~</b> 3	_	595	m)	m)	m)	ml	600
	_			605	His				610					615	
Pro	Tyr	Gly	Asp 620	Ser	Leu	Leu	Ser	Glu 625	Glu	Val	Ala	Ser	Ala 630	Leu	Ala
Glu	Leu	Leu 635	Pro	Val	Trp	Ser	Gln 640	Leu	Ile	Glu	Glu	His 645	Ser	Leu	Gln
Asp	Leu		Ala	Ser	Pro	Gln		Lys	Arg	Leu	Asp		Val	Ser	Phe
-	650	1				655		-			660				
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val
665					670					675	_	_		_	680
Ala	Asn	Gln	Ile	Thr 685	Arg	Ala	Leu	Leu	Gly 690	Val	Glu	Ala	His	Glu 695	Ile
Ser	Met	Leu	Phe 700	Leu	Thr	Asp	Tyr	Ile 705	Lys	Ser	Ala	Thr	Gly 710	Leu	Ser
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys
		715					720					725			
Thr	Gly 730	Met	Gln	Ser	Ile	Cys 735	His	Ala	Met	Ser	Lys 740	Glu	Leu	Val	Pro
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala
745					750					755					760
				765	Arg				770					775	
Lys	Val	Val	Val 780	Ser	Leu	Pro	Thr	Thr 785	Leu	Tyr	Pro	Thr	Leu 790	Thr	Phe
Ser	Pro	Pro 795	Leu	Pro	Ala	Glu	Lys 800	Gln	Ala	Leu	Ala	Glu 805	Asn	Ser	Ile
Leu	Gly 810	Tyr	Tyr	Ser	Lys	Ile 815	Val	Phe	Val	Trp	Asp 820	Lys	Pro	Trp	Trp
Arg		Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile
825					830					835					840
Ser	Phe	Ala	Arg	Asp 845	Thr	Ser	Ile	Asp	Val 850	Asp	Arg	Gln	Trp	Ser 855	Ile
Thr	Cys	Phe	Met 860	Val	Gly	Asp	Pro	Gly 865	Arg	Lys	Trp	Ser	Gln 870	Gln	Ser
Lys	Gln	Val 875		Gln	Lys	Ser	Val 880	Trp	Asp	Gln	Leu	Arg 885	Ala	Ala	Tyr
Glu			Gly	Ala	Gln	Val 895		Glu	Pro	Ala	Asn 900		Leu	Glu	Ile
Glu	890 Trn	Ser	Lve	Gln	Gln		Dhe	Gln	Glv	Δla		Ser	Δla	Val	Tvr
905	111	DCI	БуБ	0111	910	- y -	1110	0111	O <sub>T</sub>	915	110	001	1114	•41	920
	Leu	Asn	Asp	Leu 925	Ile	Thr	Leu	Gly	Ser 930	Ala	Leu	Arg	Thr	Pro 935	
Lys	Ser	Val			Val	Gly	Thr			Ser	Leu	Val	Trp		Gly
Tyr	Met		940 Gly	Ala	Ile	Arg		945 Gly	Gln	Arg	Gly			Glu	Val
77- 7	7A 7	955	T ~~~	1707	D	70.7	960					965			
val	970	ser	ьeu	vaı	Pro	975	Α⊥а								

<sup>&</sup>lt;210> 26 <211> 2976

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Unknown

<220>

<223> Barley alpha amylase signal sequence: BEST1 mature: artificial spacer: and K:trAPAO. For plant expression. <221> sig peptide <222> (1)...(72) <223> Barley alpha amylase signal sequence <221> mat peptide <222> (73)...(1545) <223> BEST1 mature <221> misc feature <222> (1546)...(1584) <223> spacer sequence <221> misc feature <222> (1585)...(2973) <223> K:trAPAO <221> CDS <222> (1)...(2973) <221> misc feature <222> (1585)...(1587) <223> Extra lysine <400> 26 atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc 48 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly -20 -15 ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc 96 Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr - 5 gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc 144 Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg 10 15 gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg 192 Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro 25 30 35 ccc caa cac gcc egg ccc tgg gcg ggc gtt egc ecc gcc acc caa ttt 240 Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe 45 50 gge tee gae tge tte gge geg gee tat ett ege aaa gge age ete gee 288 Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala 60 65 70 ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca 336 Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser 75 80 gge get aaa eee gge eag tae eee gte atg gte tgg gte tae gge gge 384 Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly

90	95		100		
ggc ttc gcc ggc Gly Phe Ala Gly 105					432
ctt gcg cga cag Leu Ala Arg Gln			r Phe Asn Tyr A		480
atc ctg ggc ttt Ile Leu Gly Phe 140	•		ı Ser Arg Glu S		528
gga act tcg ggc Gly Thr Ser Gly 155					576
tgg gtg cag agc Trp Val Gln Ser 170					624
acg gtc ttt ggt Thr Val Phe Gly 185					672
acc tcg ccg ctg Thr Ser Pro Leu		_	g Gly Ala Ile I		720
cca ggg ctg acg Pro Gly Leu Thr 220			ı Ala Asp Ser A		768
ggc gag cgc ctc Gly Glu Arg Leu 235			<b>-</b>	-	816
gcc acc ctg atg Ala Thr Leu Met 250				·	864
ctg cgc agg ccg Leu Arg Arg Pro 265					912
ccg cag acc gac Pro Gln Thr Asp			a Gly Gln Leu A		960
cgg gtc ctg atc Arg Val Leu Ile 300			ı Gly Arg Ala F		1008
cgc gcg ccg atg Arg Ala Pro Met 315					1056

1104

cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp 330 335 340

ggo Gly 345	/ Arc	g gco g Ala	c acg a Thr	g ecc Pro	aag Lys 350	Glu	atg Met	g gto Val	gcg Ala	g cgc Arg 355	j Il∈	c tto e Phe	c ggd e Gly	c gad / Asp	e aat Asn 360	1152
cag Gln	tto Phe	e aat e Asr	cgg Arg	365 365	' Val	tcg Ser	gcc Ala	ttc Phe	tcg Ser 370	Glu	ı geç	g ctt a Lei	gtg ıVal	g ego Arg 375	c cag g Gln	1200
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					ccc Pro 830											2592

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caa Gln	cga Arg	ggt Gly 955	gct Ala	gca Ala	gaa Glu	gtt Val	gtg Val 960	gct Ala	agc Ser	ctg Leu	gtg Val	cca Pro 965	gca Ala	gca Ala		2973
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	Ser			45					50					55		
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Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 625 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 640 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 655 660 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 670 675 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 685 690 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 700 705 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 720 715 725 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 740 735 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 750 755 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 765 770 775 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 780 785 790 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 800 805 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 815 820 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 830 835 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 845 850 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 865 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 880 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 895 900 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 910 915 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 925 930 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 945 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 960 <210> 28 <211> 3618 <212> DNA <213> Unknown <220> <223> gst:esp1:sp:K:trapao, 3618. 1-687, gst + polylinker; 688-2190, esp1 mat; 2191-2226 spacer; 2227-3615, K:trAPAO, 3616-3618, stop codon. For bacterial expression. <221> CDS <222> (1)...(3615) <221> misc feature

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				ccc Pro												192
				atg Met												240
				tgt Cys 85												288
				gat Asp					-	_	_		_		_	336
				act Thr												384
				ttc Phe												432
				acc Thr												480
				atg Met 165												528

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_			_	_			-			_	cag Gln				_	624
_					-					_	gat Asp 220	_	_	_	_	672
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											ctg Leu					1200
											atc Ile					1248
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			-		tcc Ser			-						_		1392
	_		_		tgg Trp 470				_		~			_		1440
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gac Asp	tcc Ser 850	ttg Leu	ctg Leu	agc Ser	gag Glu	gag Glu 855	gtt Val	gca Ala	agt Ser	gca Ala	ctt Leu 860	gcg Ala	gaa Glu	ctc Leu	ctc Leu	2592
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gat Asp	Leu	atc Ile 1155	Thr	ctg Leu	ggt Gly :	Ser 1	gcg Ala 1160	ctc Leu	aga Arg	acg Thr	ccg Pro	ttc Phe 1165	Lys	agt Ser	gtt Val	3504

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ggg gcc ata Gly Ala Ilo 1185	a cga tcg e Arg Ser	ggt caa Gly Gln 1190	cga ggt Arg Gly	gct gca Ala Ala 1195	Glu Val	gtg gct Val Ala	agc 3600 Ser 1200
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Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn 

Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly 840 Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu 855 860 Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys 870 875 Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr 890 885 Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln 900 905 Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu 920 915 925 Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe 935 940 Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met 950 955 Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val 970 965 His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys 985 Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val 1000 1005 Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro 1015 1020 Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr 1030 1035 Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln 1045 1050 Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala 1065 1060 1070 Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe 1075 1080 1085 Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val 1090 1095 1100 Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala 1110 1115 Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser 1125 1130 Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn 1145 1150 1140 Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val 1165 1155 1160 His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu 1180 1170 1175 Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser 1190 1195 Leu Val Pro Ala Ala

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<212> DNA

<213> Unknown

1205

<220>

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 1-687 gst
 + polylinker, 688-2163, BEST1 mature; 2164-2199,
 spacer, 2200-3588, K:trAPAO

	< 2	222>	(1)	(		e inke:	r									
	< 2	222>		8)	tide .(21) atur											
	< 2	222>	(21	$6\overline{4}$ ).	ature (2) seque	199)										
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		221> 222>		(:	3588)	)										
	< 2	222>	(220	00).	ature (22 ysine	202)										
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		_	_	_		gat Asp			-			_			_	144
	_					ctt Leu 55					_		_	_		192
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						aaa Lys										288
		_	_	_		aga Arg			-	-	-		-		_	336
						aaa Lys										384
_	_		-		-	gat Asp 135	-		_							432
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<i>α</i> 1	7	77.5	77-7	m1	****	D	<b>3</b>	<b>D</b> 1		_		_		_	_	
145	Asp	HIS	vaı	Thr	His 150	Pro	Asp	Pne	Met	Leu 155	Tyr	Asp	Ala	Leu	160	
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					cgt Arg											576
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					gac Asp											672
					acg Thr 230											720
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					tat Tyr											912
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ccc Pro	ggc	cag Gln	tac Tyr	ccc Pro 325	gtc Val	atg Met	gtc Val	tgg Trp	gtc Val 330	tac Tyr	ggc	ggc Gly	ggc Gly	ttc Phe 335	gcc Ala	1008
					atg Met											1056
					gtg Val											1104
					ggt Gly											1152
					ctc Leu 390											1200

ago Ser	aac Ası	c gc	c cgo a Aro	c gco g Ala 409	a Phe	e Gly	a ggg y Gly	g gad y Asp	2 CC 2 Pro 410	o Gl	c cg y Ar	a gtg g Val	g ac	g gt r Va 41	c ttt l Phe 5	1248
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ctg Leu	ago Sei	Lys 435	3 GTA	cto Leu	tto Phe	e cgt Arg	gg Gl <sub>y</sub> 440	/ Ala	ato Ile	c cto	c gaa u Gli	a agt u Sei 445	e Pro	a ggg	g ctg y Leu	1344
acg Thr	cga Arg 450	Pro	g cto Leu	gcg Ala	acg Thr	cto Leu 455	ı Ala	gac Asp	ago Ser	gco Ala	c gco a Ala 460	a Ser	Gly	gag Gli	g cgc ı Arg	1392
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ccg Pro	cgt Arg	ccg Pro	acc Thr 500	gga Gly	ccg Pro	atc Ile	gtc Val	gat Asp 505	ggc	cat His	gtg Val	ctg Leu	ccg Pro 510	Gln	acc Thr	1536
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cgg ( Arg (	Gly 999	gtc Val 595	tcg Ser	gcc Ala	ttc Phe	Ser	gaa Glu 600	gcg Ala	ctt Leu	gtg Val	cgc Arg	cag Gln 605	ggc Gly	gcg Ala	ccc Pro	1824
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gct a Ala : 625	acc Thr	cac His	gga Gly	Ala	gaa Glu 630	att Ile	ccc Pro	tac ( Tyr	Val	ttc Phe 635	gjå aaa	gtg Val	ttc Phe	aag Lys	ctc Leu 640	1920
gac g	gag	ttg	ggt (	ctg	ttc (	gat ·	tgg	ccg (		gag	aga	ccc	acg	ccc	gcc	1968

As	sp G	lu	Leu	ı Gl	y Le 64	u Ph 5	e As	p Tr	p Pr	o Pr 65	o Gl O	u Gl	y Pr	o Th	r Pr 65	o Ala	
ga As	ic c	gt rg	gcg Ala	Cte Le 66	u GI	c ca y Gl:	a ct n Le	g at u Me	g tc t Se 66	r Se	c gc r Al	c tg a Tr	g gt p Va	c cg l Ar	g Ph	c gcc e Ala	2016
aa Ly	ıg aa rs As	511	ggc Gly 675	AS	c cco p Pro	gc Ala	c ggg	g ga y As 68	p Al	c ct <sup>.</sup> a Lei	t ac u Th	c tg r Tr	g cc p Pr	o Ala	c ta a Ty	t tct r Ser	2064
ac Th	g gg r G]	- Y	aag Lys	tcg Sei	g aco	c ato	g aca Thi	r Ph	c ggt e Gly	t cco y Pro	c gag o Gli	g gg u Gl <sub>i</sub> 700	y Ar	c gcg g Ala	g gc	g gtg a Val	2112
gt Va 70	T 26	g r	ccc Pro	gga Gl}	a cct / Pro	tco Ser	: I16	e ec	c cct o Pro	t tgo Cys	g gcg 5 Ala 715	a Asp	t ggo p Gly	c gcd y Ala	c aag a Lys	g gcg s Ala 720	2160
gl gg	y Gl 9 99	y (	gga Gly	ggc	agc Ser 725	, GTA	gga Gly	a ggo Gly	c ago y Ser	ggc Gl <sub>y</sub> 730	/ Gl	a ggo / Gly	c ago / Ser	c aaa C Lys	gad Asp 735	e aac o Asn	2208
gt Vai	t gc l Al	g g a A	gac Asp	gtg Val 740	. vaı	gtg Val	gtg Val	ggc Gl <sub>y</sub>	get Ala 745	. Gly	ttg Leu	g ago 1 Ser	ggt Gly	ttg Leu 750	Glu	g acg ı Thr	2256
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ato Met	g ga As <sub>]</sub> 77	ָרַ ע	gt	gta Val	gly aaa	gga Gly	aag Lys 775	act Thr	ctg Leu	agc Ser	gta Val	caa Gln 780	Ser	ggt Gly	ccc Pro	ggc	2352
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cto Leu	cag Glr	ја n А	rg	acg Thr 820	act Thr	gga Gly	aat Asn	tca Ser	atc Ile 825	cat His	caa Gln	gca Ala	caa Gln	gac Asp 830	ggt Gly	aca Thr	2496
acc Thr	act Thr	1.	ca q hr 1 35	gct Ala	cct Pro	tat Tyr	ggt Gly	gac Asp 840	tcc Ser	ttg Leu	ctg Leu	agc Ser	gag Glu 845	gag Glu	gtt Val	gca Ala	2544
agt Ser	gca Ala 850	ъ	tt g eu <i>A</i>	gcg Ala	gaa Glu	ctc Leu	ctc Leu 855	ccc Pro	gta Val	tgg Trp	tct Ser	cag Gln 860	ctg Leu	atc Ile	gaa Glu	gag Glu	2592
cat His 865	agc Ser	ct Le	eu G	caa Sln	Asp	ctc Leu 870	aag Lys	gcg Ala	agc Ser	Pro	cag Gln 875	gcg Ala	aag Lys	cgg Arg	ctc Leu	gac Asp 880	2640
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					atg Met											2784
					att Ile											2832
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_		_			tca Ser											2928
					ggc Gly											2976
			Lys		gtg Val			Ser					Leu			3024
	_	Thr			cca Pro		Leu		_		-	Gln				3072
	Asn				ggc Gly 1030	Tyr					Val					3120
					gaa Glu 5					Gly					Ser	3168
				Ser	ttt Phe				Thr					Asp		3216
			Ile		tgt Cys			Val					Arg			3264
		Gln			cag Gln		Arg					Trp				3312
	Ala				aac Asn 111(	Ala					Pro					3360
					tgg Trp					Tyr					Pro	3408
agc	gcc	gtc	tat	aaa	ctg	aac	gat	ctc	atc	aca	ctg	ggt	tcg	gcg	ctc	3456

Ser	Ala	Val	Tyr 1140		Leu	Asn	Asp	Leu 1145		Thr	Leu	Gly	Ser 115		Leu	
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gtt Val	tgg Trp 1170	Lys	gly aaa	tat Tyr	atg Met	gaa Glu 1175	Gly	gcc Ala	ata Ile	cga Arg	tcg Ser 1180	Gly	caa Gln	cga Arg	ggt Gly	3552
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Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu 

Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr 825 Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala 835 840 845 Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu 855 860 His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp 870 875 Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala 885 890 Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu 900 905 Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala 915 920 Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr 935 940 Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys 950 955 Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile 965 970 Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val 980 985 Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro 995 1000 Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala 1015 1020 Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp 1030 1035 Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser 1045 1050 Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg 1060 1065 Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp 1075 1080 1085 Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu 1095 1100 Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn 1110 1115 Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro 1125 1130 Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu 1145 1150 Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu 1160 1165 Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly 1175 Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 1185 1190

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<sup>&</sup>lt;211> 1803

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Unknown

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

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<sup>&</sup>lt;223> Glyc(-)APAO coding sequence; mutation in putative glycosylation sites

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											gga Gly					96
		•		_				_	~	_	ggc Gly			_		144
_		-		-		_		_		_	aat Asn 60	-	-	_	_	192
	-	_	_		_				_	_	acc Thr	_				240
		-	_		_	_	_				gca Ala			-		288
_	_	_			_		_				cct Pro	-	_	_		336
											ttt Phe					384
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											gcg Ala					528
		_		_	_	_		_			ggc Gly		-			576
	-			_					_	_	aat Asn	_	_	-	_	624
											gag Glu 220					672
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			-		_	_	-	_		_	gca Ala	_	_			768

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ctgcgagctt gccttgctgc agttggagcc acttcaaacg acgtcaccaa gctcaattac
                                                                        240
tacategteg actaegeece gageaaacte acegeaattg gagatggget gaaggetace
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tttgcccttg acaggetece teettgeacg etggtgccag tgteggeett gtetteacet
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gaatacetet ttgaggttga tgecaeggeg etggtgeegg gacacaegae eecagacaae
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taatattttc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg
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acctetecce geegagaage aageattgge ggaaaattet ateetggget actatageaa
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Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
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Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
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                                    90
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
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Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
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Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
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Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
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                                        155
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
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                                    170
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
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                                185
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
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Arg Leu Phe Glu Arg Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr
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Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
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                                        235
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
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                                    250
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
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                                265
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Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala 280 His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn

125

140

220

Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser 360 365 Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly

375 380 Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val 390 395

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Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
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                                                 445
Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
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                        455
Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys
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                    470
Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
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                                     490
Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn
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                                                     510
Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
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                                                 525
Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu
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Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser
                    550
                                         555
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gageceteaa gegaageage tegaeagtgt gagettegea cactaetgtg agaaggatet
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                                                                       1080
ageccaegag atcageatge ttttteteae egaetacate aagagtgeca eeggteteag
taatattgtc tcggataaga aagacggtgg gcagtatatg cgatgcaaaa caggtgcgtg
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gecatgecat gteaaaggaa ettgtteeag geteagtgea ceteaacace ceegtegeeg
                                                                       1260
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ccattacctg	tttcatggtc	ggagacccgg	gacggaagtg	gtcccaacag	tccaagcagg	1620
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tcccagagcc	ggccaacgtg	ctcgagatcg	agtggtcgaa	gcagcagtat	ttccaaggag	1740
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cgttcaaggg	tgttcatttc	gttggaacgg	agacgtcttt	ggtttggaaa	gggtatatgg	1860
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<213> Rhinocladiella atrovirens

<400> 42

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Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
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Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
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Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                                    90
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
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Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala
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Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
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Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
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Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
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                                    170
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile
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Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
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Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr
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                                        235
Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu
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Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro
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Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His
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Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn
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Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
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Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
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Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
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Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
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Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
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Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val
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Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro
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                                     410
Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Leu Gly
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Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
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Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
                        455
Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys
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Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
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Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn
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Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu
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Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
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<212> PRT

<213> Rhinocladiella atrovirens

<400> 44

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Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys
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Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu
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Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn
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Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg
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Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr
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Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
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<210> 46

<211> 591

<212> PRT

<213> Rhinocladiella atrovirens

<400> 46

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala 10 Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr 25 Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu 55 Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr 70 75 Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu 85 90 Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro 100 105 Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr 120 Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val 135 140 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln 150 155 Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly 165 170 Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn 180 185 190 Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe 200 Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr 215 220 Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro 230 235 Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu 245 250 Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp 265 Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala

His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala 

<210> 47

<211> 600

<212> PRT

<213> Exophiala spinifera

<400> 47

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala 

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala

			עועט													
		12>	Unkn	lown												
	< 2	20> 21> 22>	CDS (1).	(1	L392)											
	<2	223>	Cys	( - )	APAC	); re	emova	ıl of	Е суя	steir	ne 46	51				
aaa Lys 1	gac	aac Asn	48 gtt Val	gcg Ala 5	gac Asp	gtg Val	gta Val	gtg Val	gtg Val 10	ggc Gly	gct Ala	ggc Gly	ttg Leu	agc Ser 15	ggt Gly	48
ttg Leu	gag Glu	acg Thr	gca Ala 20	cgc Arg	aaa Lys	gtc Val	cag Gln	gcc Ala 25	gcc Ala	ggt Gly	ctg Leu	tcc Ser	tgc Cys 30	ctc Leu	gtt Val	96
ctt Leu	gag Glu	gcg Ala 35	atg Met	gat Asp	cgt Arg	gta Val	999 Gly 40	gga Gly	aag Lys	act Thr	ctg Leu	agc Ser 45	gta Val	caa Gln	tcg Ser	144
ggt Gly	ccc Pro 50	ggc Gly	agg Arg	acg Thr	act Thr	atc Ile 55	aac Asn	gac Asp	ctc Leu	ggc Gly	gct Ala 60	gcg Ala	tgg Trp	atc Ile	aat Asn	192
gac Asp 65	agc Ser	aac Asn	caa Gln	agc Ser	gaa Glu 70	gta Val	tcc Ser	aga Arg	ttg Leu	ttt Phe 75	gaa Glu	aga Arg	ttt Phe	cat His	ttg Leu 80	240
gag Glu	ggc Gly	gag Glu	ctc Leu	cag Gln 85	agg Arg	acg Thr	act Thr	gga Gly	aat Asn 90	tca Ser	atc Ile	cat His	caa Gln	gca Ala 95	caa Gln	288
gac Asp	ggt Gly	aca Thr	acc Thr 100	act Thr	aca Thr	gct Ala	cct Pro	tat Tyr 105	ggt Gly	gac Asp	tcc Ser	ttg Leu	ctg Leu 110	agc Ser	gag Glu	336
gag Glu	gtt Val	gca Ala 115	agt Ser	gca Ala	ctt Leu	gcg Ala	gaa Glu 120	ctc Leu	ctc Leu	ccc Pro	gta Val	tgg Trp 125	tct Ser	cag Gln	ctg Leu	384
atc Ile	gaa Glu 130	gag Glu	cat His	agc Ser	ctt Leu	caa Gln 135	gac Asp	ctc Leu	aag Lys	gcg Ala	agc Ser 140	cct Pro	cag Gln	gcg Ala	aag Lys	432
cgg Arg 145	ctc Leu	gac Asp	agt Ser	gtg Val	agc Ser 150	ttc Phe	gcg Ala	cac His	tac Tyr	tgt Cys 155	gag Glu	aag Lys	gaa Glu	cta Leu	aac Asn 160	480
ttg Leu	cct Pro	gct Ala	gtt Val	ctc Leu 165	ggc	gta Val	gca Ala	aac Asn	cag Gln 170	atc Ile	aca Thr	cgc Arg	gct Ala	ctg Leu 175	ctc Leu	528
ggt Gly	gtg Val	gaa Glu	gcc Ala 180	cac His	gag Glu	atc Ile	agc Ser	atg Met 185	Leu	ttt Phe	ctc Leu	acc Thr	gac Asp 190	tac Tyr	atc Ile	576
aag Lys	agt Ser	gcc Ala	acc Thr	ggt Gly	ctc Leu	agt Ser	aat Asn 200	Ile	ttc Phe	tcg Ser	gac Asp	aag Lys 205	aaa Lys	gac Asp	ggc	624

	_		_	_		aaa Lys 215			_	_	_		_		_	672
						cca Pro										720
_	_			_	_	gca Ala			_		_	_	_	_		768
						aaa Lys										816
_				_		ttt Phe						_		_		864
-	_		_			atc Ile 295	_					_				912
						tgg Trp										960
	_	_		_		atc Ile			_	_	_		_		_	1008
_	_	_				att Ile		_		_	_					1056
	_				_	tcc Ser	_	-	-	-		_		_		1104
_			_	_	_	tac Tyr 375			_		_		-			1152
_	-				-	atc Ile			_	_	_	_				1200
	_	_	_	_	_	tat Tyr		_		_				_		1248
_			_	_	_	ttc Phe	-	_	_			_		_		1296
						gjå aaa										1344
caa	cga	ggt	gct	gca	gaa	gtt	gtg	gct	agc	ctg	gtg	сса	gca	gca	tag	1392

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala \* 450 460

<210> 49 <211> 463 <212> PRT <213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteine 461

<400> 49 Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 40 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 55 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 70 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 100 105 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 135 140 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 150 155 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 185 180 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 200 195 205 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 215 220 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 230 235 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 250 245 Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr 265 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 280 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 295 300 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 310 315 Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 360 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 375

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln

205					200					395					400	
385 Gly	Ala	Pro	Ser	Ala 405	390 Val	Tyr	Gly	Leu	Asn 410		Leu	Ile	Thr	Leu 415		
			420	Thr				Ser 425	Val				430			
		435					440	Met				445			Gly	
Gln	Arg 450	Gly	Ala	Ala	Glu	Val 455	Val	Ala	Ser	Leu	Val 460	Pro	Ala	Ala		
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	<2 <2	220> 221> 222>	(1).													
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ttg Leu	gag Glu	acg Thr	gca Ala 20	cgc Arg	aaa Lys	gtc Val	cag Gln	gcc Ala 25	gcc Ala	ggt Gly	ctg Leu	tcc Ser	tgc Cys 30	ctc Leu	gtt Val	96
ctt Leu	gag Glu	gcg Ala 35	atg Met	gat Asp	cgt Arg	gta Val	ggg Gly 40	gga Gly	aag Lys	act Thr	ctg Leu	agc Ser 45	gta Val	caa Gln	tcg Ser	144
ggt Gly	ccc Pro 50	ggc	agg Arg	acg Thr	act Thr	atc Ile 55	aac Asn	gac Asp	ctc Leu	ggc Gly	gct Ala 60	gcg Ala	tgg Trp	atc Ile	aat Asn	192
gac Asp 65	agc Ser	aac Asn	caa Gln	agc Ser	gaa Glu 70	gta Val	tcc Ser	aga Arg	ttg Leu	ttt Phe 75	gaa Glu	aga Arg	ttt Phe	cat His	ttg Leu 80	240
gag Glu	ggc	gag Glu	ctc Leu	cag Gln 85	Arg	acg Thr	act Thr	gga Gly	aat Asn 90	tca Ser	atc Ile	cat His	caa Gln	gca Ala 95	caa Gln	288
gac Asp	ggt Gly	aca Thr	acc Thr 100	act Thr	aca Thr	gct Ala	cct Pro	tat Tyr 105	Gly	gac Asp	tcc Ser	ttg Leu	ctg Leu 110	Ser	gag Glu	336
gag Glu	gtt Val	gca Ala 115	Ser	gca Ala	ctt Leu	gcg Ala	gaa Glu 120	Leu	ctc Leu	ccc Pro	gta Val	tgg Trp 125	Ser	cag Gln	ctg Leu	384
atc Ile	gaa Glu 130	Glu	cat His	ago Ser	ctt Leu	caa Gln 135	Asp	ctc Leu	aag Lys	gcg Ala	agc Ser 140	Pro	cag Gln	gcg Ala	aag Lys	432
cgg Arg 145	Leu	gac Asp	agt Ser	gtg Val	g ago Ser 150	Phe	gcg	g cac His	tac Tyr	tgt Cys 155	Glu	aag Lys	gaa Glu	cta Lev	a aac a Asn 160	480

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ggt Gly	gtg Val	gaa Glu	gcc Ala 180	cac His	gag Glu	atc Ile	agc Ser	atg Met 185	ctt Leu	ttt Phe	ctc Leu	acc Thr	gac Asp 190	tac Tyr	atc Ile	576
aag Lys	agt Ser	gcc Ala 195	acc Thr	ggt Gly	ctc Leu	agt Ser	aat Asn 200	att Ile	ttc Phe	tcg Ser	gac Asp	aag Lys 205	aaa Lys	gac Asp	ggc	624
gly aaa	cag Gln 210	tat Tyr	atg Met	cga Arg	tgc Cys	aaa Lys 215	aca Thr	ggt Gly	atg Met	cag Gln	tcg Ser 220	att Ile	tcg Ser	cat His	gcc Ala	672
atg Met 225	tca Ser	aag Lys	gaa Glu	ctt Leu	gtt Val 230	cca Pro	ggc Gly	tca Ser	gtg Val	cac His 235	ctc Leu	aac Asn	acc Thr	ccc Pro	gtc Val 240	720
gct Ala	gaa Glu	att Ile	gag Glu	cag Gln 245	tcg Ser	gca Ala	tcc Ser	ggc Gly	tgt Cys 250	aca Thr	gta Val	cga Arg	tcg Ser	gcc Ala 255	tcg Ser	768
ggc Gly	gcc Ala	gtg Val	ttc Phe 260	cga Arg	agc Ser	aaa Lys	aag Lys	gtg Val 265	gtg Val	gtt Val	tcg Ser	tta Leu	ccg Pro 270	aca Thr	acc Thr	816
ttg Leu	tat Tyr	ccc Pro 275	acc Thr	ttg Leu	aca Thr	ttt Phe	tca Ser 280	cca Pro	cct Pro	ctt Leu	ccc Pro	gcc Ala 285	gag Glu	aag Lys	caa Gln	864
gca Ala	ttg Leu 290	gcg Ala	gaa Glu	aat Asn	tct Ser	atc Ile 295	ctg Leu	ggc Gly	tac Tyr	tat Tyr	agc Ser 300	aag Lys	ata Ile	gtc Val	ttc Phe	912
gta Val 305	tgg Trp	gac Asp	aag Lys	ccg Pro	tgg Trp 310	tgg Trp	cgc Arg	gaa Glu	caa Gln	ggc Gly 315	ttc Phe	tcg Ser	ggc Gly	gtc Val	ctc Leu 320	960
caa Gln	tcg Ser	agc Ser	tcc Ser	gac Asp 325	ccc Pro	atc Ile	tca Ser	ttt Phe	gcc Ala 330	aga Arg	gat Asp	acc Thr	agc Ser	atc Ile 335	gac Asp	1008
gtc Val	gat Asp	cga Arg	caa Gln 340	tgg Trp	tcc Ser	att Ile	acc Thr	tgt Cys 345	ttc Phe	atg Met	gtc Val	gga Gly	gac Asp 350	Pro	gga Gly	1056
cgg Arg	aag Lys	tgg Trp 355	Ser	caa Gln	cag Gln	tcc Ser	aag Lys 360	Gln	gta Val	cga Arg	caa Gln	aag Lys 365	Ser	gtc Val	tgg Trp	1104
gac Asp	caa Gln 370	Leu	cgc Arg	gca Ala	gcc Ala	tac Tyr 375	Glu	aac Asn	gcc Ala	gly	gcc Ala 380	Gln	gto Val	cca Pro	gag Glu	1152
ccg Pro 385	Ala	aac Asn	gtg Val	cto Leu	gaa Glu 390	Ile	gag Glu	tgg Trp	tcg Ser	aag Lys 395	Gln	cag Gln	tat Tyr	ttc Phe	caa Gln 400	1200
gga Gly	gct Ala	ccg	g ago Ser	gcc Ala	gtc Val	tat Tyr	. GJÀ : aaa	rctg Leu	aac Asn	gat Asp	cto Leu	ato Ile	aca Thr	ctg Lev	ggt Gly	1248

405 410 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu

420

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly

435

440

1392

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<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

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Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu

165
170
175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly

195 200 205 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser

245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300

Val 305																
		Asp	Lys	Pro	Trp 310	Trp	Arg	Glu	Gln	Gly 315	Phe	Ser	Gly	Val	Leu 320	
		Ser	Ser	Asp		Ile	Ser	Phe	Ala 330		Asp	Thr	Ser	Ile 335		
Val	Asp	Arg	Gln 340		Ser	Ile	Thr	Cys 345		Met	Val	Gly	Asp		Gly	
Arg	Lys	Trp		Gln	Gln	Ser	Lys 360		Val	Arg	Gln	Lys 365		Val	Trp	
Asp	Gln 370		Arg	Ala	Ala	Tyr 375		Asn	Ala	Gly	Ala 380		Val	Pro	Glu	
Pro 385		Asn	Val	Leu	Glu 390		Glu	Trp	Ser	Lys 395	Gln	Gln	Tyr	Phe	Gln 400	
	Ala	Pro	Ser	Ala 405		Tyr	Gly	Leu	Asn 410		Leu	Ile	Thr	Leu 415		
Ser	Ala	Leu	Arg 420		Pro	Phe	Lys	Ser 425		His	Phe	Val	Gly 430		Glu	
Thr	Ser	Leu 435		Trp	Lys	Gly	Tyr 440		Glu	Gly	Ala	Ile 445		Ser	Gly	
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		210>		,												
	<2	212>	1392 DNA Unkr													
		220>	an a													
		221>	(1).	(1	L392)	ı										
	<2	223>	Cys 461	( - )	APAC	); re	emova	al of	E cys	steir	nes 1	69,	359,	and	f	
222	< 4															
	000	100>		aaa	<b>a</b> 2.a	~+ <i>~</i>	~+ ·	~+~~	ata	~~~	~at	~~~	++~	200	~~+	4.0
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1 ttg Leu ctt	Asp gag Glu gag	aac Asn acg Thr	gtt Val gca Ala 20 atg	Ala 5 cgc Arg	Asp aaa Lys cgt	Val gtc Val gta	Val cag Gln ggg	yal gcc Ala 25 gga	Val 10 gcc Ala aag	Gly ggt Gly act	Ala ctg Leu	agc Ser	tcc Ser 30	Ser 15 ctc Leu caa	gtt Val tcg	
ttg Leu ctt Leu	Asp gag Glu gag Glu	aac Asn acg Thr gcg Ala 35	gtt Val gca Ala 20 atg Met	Ala 5 cgc Arg gat Asp	Asp aaa Lys cgt Arg	yal gtc val gta val	Cag Gln ggg Gly 40	yal gcc Ala 25 gga Gly	Val 10 gcc Ala aag Lys	Gly ggt Gly act Thr	Ala ctg Leu ctg	agc ser agc ser 45	tcc ser 30 gta Val	Ser 15 ctc Leu caa Gln	gtt Val tcg ser	96
ttg Leu ctt Leu ggt Gly	gag Glu gag Glu ccc Pro 50	aac Asn acg Thr gcg Ala 35 ggc Gly	gca Ala 20 atg Met agg Arg	Ala 5 cgc Arg gat Asp acg Thr	Asp aaa Lys cgt Arg act Thr	yal gtc val gta val atc Ile 55	cag Gln 999 Gly 40 aac Asn	gcc Ala 25 gga Gly gac Asp	Val 10 gcc Ala aag Lys ctc Leu	Gly ggt Gly act Thr ggc Gly	Ala ctg Leu ctg Leu gct Ala	agc Ser agc Ser 45 gcg Ala	tcc ser 30 gta Val tgg Trp	Ser 15 ctc Leu caa Gln atc Ile	gtt Val tcg Ser aat Asn	96 144
tttg Leu ctt Leu ggt Gly gac Asp 65	gag Glu gag Glu ccc Pro 50 agc Ser	aac Asn acg Thr gcg Ala 35 ggc Gly aac Asn	gtt Val gca Ala 20 atg Met agg Arg caa Gln	Ala 5 cgc Arg gat Asp acg Thr agc ser cag	Asp aaa Lys cgt Arg act Thr gaa Glu 70 agg	yal gtc Val gta Val atc Ile 55 gta Val acg	cag Gln ggg Gly 40 aac Asn tcc Ser	gcc Ala 25 gga Gly gac Asp aga Arg	Val 10 gcc Ala aag Lys ctc Leu ttg Leu aat	ggt Gly act Thr ggc Gly ttt Phe 75 tca	Ctg Leu Ctg Leu gct Ala 60 gaa	agc Ser agc Ser 45 gcg Ala aga Arg	tcc ser 30 gta Val tgg Trp ttt Phe	Ser 15 ctc Leu caa Gln atc Ile cat His	gtt Val tcg Ser aat Asn ttg Leu 80	96 144 192

gag Glu	gtt Val	gca Ala 115	agt Ser	gca Ala	ctt Leu	gcg Ala	gaa Glu 120	ctc Leu	ctc Leu	ccc Pro	gta Val	tgg Trp 125	tct Ser	cag Gln	ctg Leu	384
atc Ile	gaa Glu 130	gag Glu	cat His	agc Ser	ctt Leu	caa Gln 135	gac Asp	ctc Leu	aag Lys	gcg Ala	agc Ser 140	cct Pro	cag Gln	gcg Ala	aag Lys	432
	ctc Leu														aac Asn 160	480
	cct Pro															528
	gtg Val															576
	agt Ser															624
	cag Gln 210															672
atg Met 225	tca Ser	aag Lys	gaa Glu	ctt Leu	gtt Val 230	cca Pro	gly ggc	tca Ser	gtg Val	cac His 235	ctc Leu	aac Asn	acc Thr	ccc Pro	gtc Val 240	720
gct Ala	gaa Glu	att Ile	gag Glu	cag Gln 245	tcg Ser	gca Ala	tcc Ser	ggc gly	tgt Cys 250	aca Thr	gta Val	cga Arg	tcg Ser	gcc Ala 255	tcg Ser	768
ggc Gly	gcc Ala	gtg Val	ttc Phe 260	cga Arg	agc Ser	aaa Lys	aag Lys	gtg Val 265	gtg Val	gtt Val	tcg Ser	tta Leu	ccg Pro 270	aca Thr	acc Thr	816
ttg Leu	tat Tyr	ccc Pro 275	acc Thr	ttg Leu	aca Thr	ttt Phe	tca Ser 280	cca Pro	cct Pro	ctt Leu	ccc Pro	gcc Ala 285	gag Glu	aag Lys	caa Gln	864
	ttg Leu 290															912
	tgg Trp															960
	tcg Ser															1008
gtc Val	gat Asp	cga Arg	caa Gln 340	tgg Trp	tcc Ser	att Ile	acc Thr	tgt Cys 345	ttc Phe	atg Met	gtc Val	gga Gly	gac Asp 350	ccg Pro	gga Gly	1056
cgg Arg	aag Lys	tgg Trp	tcc Ser	caa Gln	cag Gln	tcc Ser	aag Lys	cag Gln	gta Val	cga Arg	caa Gln	aag Lys	tct Ser	gtc Val	tgg Trp	1104

355 360 365

gae caa ete ege gea gee tae gag aac gee ggg gee caa gte eea gag 1152 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag tat ttc caa 1200 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 390 gga get eeg age gee gte tat ggg etg aac gat ete ate aca etg ggt 1248 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 410 teg geg ete aga aeg eeg tte aag agt gtt eat tte gtt gga aeg gag 1296 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu acg tet tta gtt tgg aaa ggg tat atg gaa ggg gee ata ega teg ggt 1344 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala \* 455

<210> 53

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 169, 359, and 461

<400> 53 Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val 25 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 40 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 55 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 70 75 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 90 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 105 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 120 125 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys

130 135 140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile

180 185 190 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly

